

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/813, 775-A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 ☐ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.

- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 ☐ PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.

- 7 ☐ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 ☐ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 ☐ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ☒ Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

- 11 ☒ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 ☐ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

DATE: 06/28/2001

PATENT APPLICATION: US/09/813,775A

TIME: 16:25:27

Input Set : A:\GENENT.57CP2new.txt

Output Set: N:\CRF3\06282001\I813775A.raw

Does Not Comply
Corrected Diskette Needed

see p.5

```

4 <110> APPLICANT: DeSauvage, Frederick
5   Henner, Dennis, J.
7 <120> TITLE OF INVENTION: Novel chimpanzee erythropoietin
8   polypeptides and nucleic acids encoding the same
11 <130> FILE REFERENCE: GENENT.057CP2
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/813,775A
C--> 13 <141> CURRENT FILING DATE: 2001-03-20
13 <150> PRIOR APPLICATION NUMBER: US 09/307307
14 <151> PRIOR FILING DATE: 1999-05-07
16 <150> PRIOR APPLICATION NUMBER: US 09/552265
17 <151> PRIOR FILING DATE: 2000-04-19
19 <160> NUMBER OF SEQ ID NOS: 52
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2329
25 <212> TYPE: DNA
26 <213> ORGANISM: Pan troglodytes
28 <220> FEATURE:
29 <221> NAME/KEY: misc_feature
30 <222> LOCATION: (1)...(2329)
31 <223> OTHER INFORMATION: n = a, t, c or g
33 <400> SEQUENCE: 1
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35 cccgggatga gggcccccgg tgtggtcacc cgccgcgccc caggtcgctg agggaccccg    120
36 gccaggcgcg gagatggggg tgcacggtga gtactcgcg gctgggcgct cccgcccgcg    180
37 cgggtccctg tttgagcggg gatttagcgc cggggctatt ggccgggagg tggctggggt    240
38 caaggaccgg cgaacttgtca aggaccccgg aagggggagg ggggtggggc agcctccacg    300
39 tgccagcggg gacttggggg agtccttggg gatggcaaaa acctgacctg tgaaggggac    360
40 acagtttggg ggttgagggg aagaaggttt gggggttctg ctgtgccagt ggagaggaag    420
W--> 41 ctgataagct gataacctgg gcgctggagc caccacttat ctgccagagg gnnntggta    480
42 gctgggggtg ggggtgtcac acggcagcag gattgaatga aggccaggga ggcagcacct    540
43 gagtgccttg atggttgggg acaggaagga cgagctgggg cagagacgtg gggatgaagg    600
44 aagctgtcct tccacagcca ccttctctcc tcccgcctg actctcagcc tggctatctc    660
45 ttctagaatg tctgtcctgg ctgtggcttc tctgtccct gctgtcgctc cctctgggcc    720
46 tcccagtcct gggcgcccca ccacgcctca tctgtgacag ccgagtcctg gagaggtacc    780
47 tcttgagggc caaggaggcc gagaatatca cggtagagac ccttccccag cacattccac    840
48 agaactcacg ctcagggctt cagggaactc ctcccagatc caggaaacctg gcacttggtt    900
49 tgggggtggg ttgggaagct agacactgcc cccctacata agaataagtc tgggtggccc    960
50 aaaccatacc tggaaactag gcaaggagca aagccagcag atcctacggc ctgtgggcca    1020
51 gggccagagc cttcagggac ccttgactcc cgggctgtg tgcatttcag acgggctgtg    1080
52 ccgaacactg cagcttgaat gagaatatca ctgtcccaga cacaaagt t aatttctatg    1140
53 cctggaagag gatggagggt agttcctttt tttttttttt tcctttcttt tggagaatct    1200
54 catttgcgag cctgattttg gatgaaaggg agaatgatcg agggaaagg taaaatggagc    1260
55 agcagagatg aggtgcctg ggcgcagagg ctcacgtcta taatcccagg ctgagatggc    1320
56 cgagatggga gaattgcttg agccctggag ttccagacca acctgggcag catagtgaga    1380
57 tcccccatct ctacaaacat ttaaaaaaat tagtcagggt aggtggtgca tgggtgtagt    1440
58 cccagatatt tggaaggctg aggcgggagg atcgcttgag ccaggaatt tgaggctgca    1500

```

RAW SEQUENCE LISTING

DATE: 06/28/2001

PATENT APPLICATION: US/09/813,775A

TIME: 16:25:27

Input Set : A:\GENENT.57CP2new.txt

Output Set: N:\CRF3\06282001\I813775A.raw

```

59 gtgagctgtg atcacaccac tgcactccag cctcagtgac agagtgaggc cctgtctcaa 1560
60 aaaagaaaag aaaaaagaaa aataatgagg gctgtatgga atacattcat tattcattca 1620
W--> 61 ctcaactcatt cattcattca ttcatcnnn nnntcttatt gcataacctt gtttgtcag 1680
62 cttggtgctt ggggctgctg aggggcagga gggagagggg ggcattgggt agctgactcc 1740
63 cagagtccac tccctgtagg tcaggcagca ggccgtagaa gtctggcagg gcctggccct 1800
64 gctctcgga gctgtcctgc ggggccaggc cctgttggtc aactcttccc agccgtggga 1860
65 gccctgcag ctgcatgtgg ataaagccgt cagtggcctt cgcagcctca ccactctgct 1920
66 tcgggctctg ggagcccagg tgagtaggag cggacacttc tgcttgccct ttctgtaaga 1980
67 aagggagaa ggtcttgcta aggagtacag gaactgtccg tattccttcc ccttctgtgg 2040
68 cactgcagcg acctcctggt ttctccttgg cagaaggaag ccatctcccc tccagatgcg 2100
69 gcctcagctg ctccactccg aacaatcact gctgacactt tccgcaaact cttccgagtc 2160
70 tactccaatt tcctccgggg aaagctgaag ctgtacacag gggaggcctg caggacaggg 2220
71 gacagatgac caggtgtgtc cacctgggca tatccaccac ctccctcacc aacattgctt 2280
72 gtgccacacc ctccccgcc actcctgaac cccgtcgagg agctctcag 2329
74 <210> SEQ ID NO: 2
75 <211> LENGTH: 193
76 <212> TYPE: PRT
77 <213> ORGANISM: Pan troglodytes
79 <400> SEQUENCE: 2
80 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
81 1 5 10 15
82 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
83 20 25 30
84 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
85 35 40 45
86 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
87 50 55 60
88 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
89 65 70 75 80
90 Met Glu Val Arg Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
91 85 90 95
92 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
93 100 105 110
94 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
95 115 120 125
96 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
97 130 135 140
98 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
99 145 150 155 160
100 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
101 165 170 175
102 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
103 180 185 190
104 Arg
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 585
108 <212> TYPE: DNA
109 <213> ORGANISM: Pan troglodytes
111 <400> SEQUENCE: 3

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RAW SEQUENCE LISTING

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Input Set : A:\GENENT.57CP2new.txt

Output Set: N:\CRF3\06282001\I813775A.raw

```

112 atgggggtgc acgaatgtcc tgcctggctg tggtttctcc tgtccctgct gtcgctccct 60
113 ctgggcctcc cagtcctggg cgccccacca cgctcatct gtgacagccg agtcctggag 120
114 aggtacctct tggaggccaa ggaggccgag aatatcacga cgggctgtgc cgaacactgc 180
115 agcttgaatg agaatatcac tgtcccagac accaaagtta atttctatgc ctggaagagg 240
116 atggaggtca ggcagcaggc cgtagaagtc tggcagggcc tggccctgct ctcggaagct 300
117 gtcctgcggg gccaggccct gttgggtcaac tcttcccagc cgtgggagcc cctgcagctg 360
118 catgtggata aagccgtcag tggccttcgc agcctcacca ctctgcttcg ggctctggga 420
119 gccagaagg aagccatctc cctccagat gcggcctcag ctgctccact ccgaacaatc 480
120 actgctgaca ctttccgcaa actcttccga gtctactcca atttccctcg gggaaagctg 540
121 aagctgtaca caggggaggc ctgcaggaca ggggacagat gacca 585

```

123 <210> SEQ ID NO: 4

124 <211> LENGTH: 193

125 <212> TYPE: PRT

126 <213> ORGANISM: Homo sapiens

128 <400> SEQUENCE: 4

129 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu

130 1 5 10 15

131 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu

132 20 25 30

133 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu

134 35 40 45

135 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu

136 50 55 60

137 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg

138 65 70 75 80

139 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu

140 85 90 95

141 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser

142 100 105 110

143 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly

144 115 120 125

145 Leu Arg Ser Leu Thr Thr Leu Arg Ala Leu Gly Ala Gln Lys Glu

146 130 135 140

147 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile

148 145 150 155 160

149 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu

150 165 170 175

151 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

152 180 185 190

153 Arg

155 <210> SEQ ID NO: 5

156 <211> LENGTH: 193

157 <212> TYPE: PRT

158 <213> ORGANISM: Pan troglodytes

160 <400> SEQUENCE: 5

161 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu

162 1 5 10 15

163 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu

164 20 25 30

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Input Set : A:\GENENT.57CP2new.txt

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```

165 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
166      35                      40                      45
167 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
168      50                      55                      60
169 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
170 65                      70                      75                      80
171 Met Glu Val Arg Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
172      85                      90                      95
173 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
174      100                     105                     110
175 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
176      115                     120                     125
177 Leu Arg Ser Leu Thr Thr Leu Arg Ala Leu Gly Ala Lys Lys Glu
178      130                     135                     140
179 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
180 145                     150                     155                     160
181 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
182      165                     170                     175
183 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
184      180                     185                     190

```

185 Arg

187 <210> SEQ ID NO: 6

188 <211> LENGTH: 4

189 <212> TYPE: PRT

190 <213> ORGANISM: Pan troglodytes

192 <400> SEQUENCE: 6

193 Met Glu Val Arg

194 1

195 <210> SEQ ID NO: 7

196 <211> LENGTH: 4

197 <212> TYPE: PRT

198 <213> ORGANISM: Pan troglodytes

200 <220> FEATURE:

201 <221> NAME/KEY: UNSURE

202 <222> LOCATION: 2, 4

203 <223> OTHER INFORMATION: Xaa = unknown amino acid

205 <400> SEQUENCE: 7

W--> 206 Asn Xaa Ser Xaa

207 1

208 <210> SEQ ID NO: 8

209 <211> LENGTH: 4

210 <212> TYPE: PRT

211 <213> ORGANISM: Pan troglodytes

213 <220> FEATURE:

214 <221> NAME/KEY: UNSURE

215 <222> LOCATION: 2, 4

216 <223> OTHER INFORMATION: Xaa = unknown amino acid

218 <400> SEQUENCE: 8

W--> 219 Asn Xaa Thr Xaa

RAW SEQUENCE LISTING

DATE: 06/28/2001

PATENT APPLICATION: US/09/813,775A

TIME: 16:25:27

Input Set : A:\GENENT.57CP2new.txt

Output Set: N:\CRF3\06282001\I813775A.raw

220 1
 221 <210> SEQ ID NO: 9
 222 <211> LENGTH: 4
 223 <212> TYPE: PRT
 224 <213> ORGANISM: Pan troglodytes
 226 <400> SEQUENCE: 9
 227 Glu Val Arg Gln
 228 1
 229 <210> SEQ ID NO: 10
 230 <211> LENGTH: 4
 231 <212> TYPE: PRT
 232 <213> ORGANISM: Pan troglodytes
 234 <400> SEQUENCE: 10
 235 Val Arg Gln Gln
 236 1
 237 <210> SEQ ID NO: 11
 238 <211> LENGTH: 4
 239 <212> TYPE: PRT
 240 <213> ORGANISM: Pan troglodytes
 242 <400> SEQUENCE: 11
 243 Arg Gln Gln Ala
 244 1
 245 <210> SEQ ID NO: 12
 246 <211> LENGTH: 18
 247 <212> TYPE: DNA
 248 <213> ORGANISM: synthetic
 250 <400> SEQUENCE: 12
 251 accgcgccccc ctggacag
 253 <210> SEQ ID NO: 13
 254 <211> LENGTH: 25
 255 <212> TYPE: DNA
 256 <213> ORGANISM: synthetic
 258 <400> SEQUENCE: 13
 259 catccacttc tccggccaaa cttea
 261 <210> SEQ ID NO: 14
 262 <211> LENGTH: 21
 263 <212> TYPE: DNA
 264 <213> ORGANISM: synthetic
 266 <400> SEQUENCE: 14
 267 tttggccgga gaagtggatg c
 269 <210> SEQ ID NO: 15
 270 <211> LENGTH: 31
 271 <212> TYPE: DNA
 272 <213> ORGANISM: synthetic
 274 <400> SEQUENCE: 15
 275 tcactcactc actcattcat tcattcattc a
 277 <210> SEQ ID NO: 16
 278 <211> LENGTH: 29
 279 <212> TYPE: DNA

Valid <213> responses:
 - Genus species of organism
 - Unknown
 - Artificial sequence²⁵

Artificial and Unknown
 must have <220>, <223>²¹
 features to explain the
 source of the genetic
 material in the sequence.³¹

See #'s 10 and 11 on the
 Error Summary sheet.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

6/28/01

F.Y.I. →
 file://C:\C

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/813,775A

DATE: 06/28/2001

TIME: 16:25:28

Input Set : A:\GENENT.57CP2new.txt

Output Set: N:\CRF3\06282001\I813775A.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:475 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:842 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:916 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1027 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:1360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49

09/813,775

insert closing bracket

insert a hard return after each response

~~SEQUENCE LISTING~~ <110>DeSavauge, Frederick Henner, Dennis, J. <120>Novel
chimpanzee

erythropoietin polypeptides and nucleic acids encoding the same <130>

GENENT.057CP2 <150>US

09/307307 <151 1999-05-07 <150 US 09/552265 <151 2000-04-19 <160 52 <170 FastSEQ
for

Windows Version 4.0 <210 1 <211 2329 <212 DNA <213 Pan troglodytes <220 <221
misc_feature

<222 (1)...(2329) <223 n = a, t, c or g <400 1 ccccctggac agccgccctc tcctccaggc
ccgtggggct

ggccctgcac cgccgagctt 60 cccgggatga gggcccccgg tgtggtcacc cggcgcgccc caggtcgctg
agggaccccg 120

gccaggcgcg gagatggggg tgcacggtga gtactcgcgg gctgggagct cccgcccggc 180 cgggtccctg
tttgagcggg

gatttagcgc cggggctatt ggccgggagg tggctgggtt 240 caaggaccgg cgacttgtca aggaccccg
aagggggagg

ggggtggggc agcctccacg 300 tgccagcggg gacttggggg agtccttggg gatggcaaaa acctgacctg
tgaaggggac 360

acagtttggg ggttgagggg aagaagggtt ggggggttctg ctgtgccagt ggagaggaag 420 ctgataagct

sample of submitted file

major format error